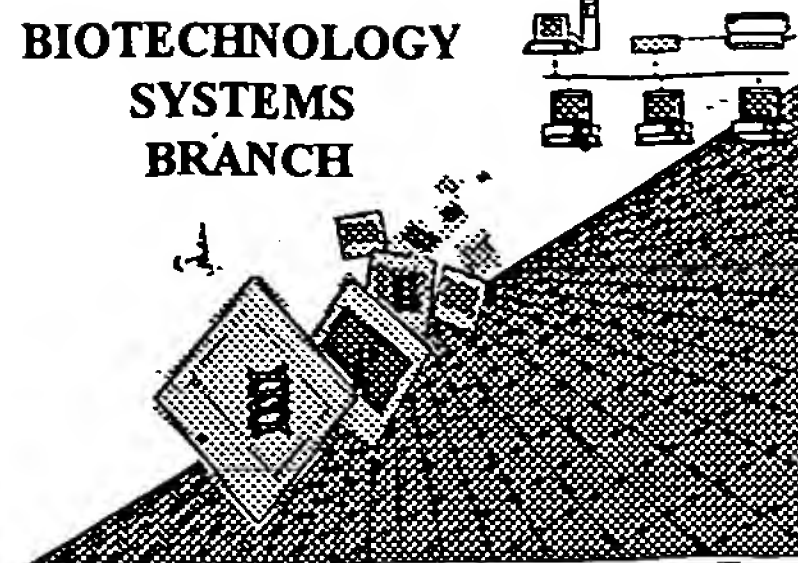


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/831,621
Source: PCT/09
Date Processed by STIC: 10/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,621

DATE: 10/11/2001

TIME: 10:39:22

Input Set : A:\98,664-A.seq list.txt

Output Set: N:\CRF3\10112001\I831621.raw

Does Not Comply
Corrected Diskette Needed

Mr 1-2

3 <110> APPLICANT: Baum, Peter
 4 DuBose, Robert
 5 Sims, John E
 6 Youakim, Adel
 7 Hasel, Karl W
 8 Hilbush, Brian S
 10 <120> TITLE OF INVENTION: Novel DNAs and Polypeptides
 12 <130> FILE REFERENCE: 98,664-A
 14 <140> CURRENT APPLICATION NUMBER: US/09/831,621
 15 <141> CURRENT FILING DATE: 1999-11-10
 17 <150> PRIOR APPLICATION NUMBER: 60/107821
 18 <151> PRIOR FILING DATE: 1998-11-10
 20 <160> NUMBER OF SEQ ID NOS: 33
 22 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

125 <210> SEQ ID NO: 9
 126 <211> LENGTH: 180 170 shown
 127 <212> TYPE: DNA
 128 <213> ORGANISM: Homo sapiens
 130 <400> SEQUENCE: 9
 131 cggctgcttg cctttttttc tgatccagac cctcggcacc tgctacttac caactggaaa 60
 132 attttacgca tcccatgaag cccagataca caaaattcca ccccatgatc aagaatcctg 120
 E--> 133 ctccactaag aatggtgcta aagtaaaact agtttaataa gccctaaaaa 180 170
 145 <210> SEQ ID NO: 11
 146 <211> LENGTH: 569
 147 <212> TYPE: DNA
 148 <213> ORGANISM: Homo sapiens
 150 <400> SEQUENCE: 11
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 152 gctttcatgc taattttctg actgtttact taccgggtaa gagcgatggg actgttttca 120
 153 ttggttggtt ctcacatact ctctgggaag tttgggttct caggacacac tgctcctcag 180
 154 ctggggacca tggccatggc ccaccacctg cccttcagtg ttcaagcagg ggacatgcac 240
 155 ccttttagtaa cctggagggg acccatcaca tgacaaccac cccaacgacc atcatcagga 300
 156 agccgctgcc tgactgagat atgccccag gaggacaagg gagagtggat gctggaaaga 360
 157 cagggcaggg gaccatcacc agggaaagac ttcattcttc ggaggacatt gaacctgggg 420
 158 ctgggtctgt agtggagccg ctgtttcttc tctgtatcc aactgttcta actcttgggc 480
 E--> 159 tttctccatt ttcagctctt tcttttctctg gcctttctcat tgctgggtcc ttcaagcctc 540
 E--> 160 cttctatnc ttccgncaat atattcttt 569
 182 <210> SEQ ID NO: 13
 183 <211> LENGTH: 618
 184 <212> TYPE: DNA
 185 <213> ORGANISM: Homo sapiens
 187 <400> SEQUENCE: 13
 188 cacgagctgt ctggttatta tacagacgca taactggagg tgggatccac acagctcaga 60

> see
 > item 9
 on
 Error
 Summary
 sheet

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,621

DATE: 10/11/2001

TIME: 10:39:22

Input Set : A:\98,664-A.seq list.txt

Output Set: N:\CRF3\10112001\I831621.raw

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189 acagctggat cttgctcagt ctctgccagg ggaagattcc ttggaggagg ccctgcagcg 120
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191 tccttggtgt gggagtgagg gcagaggaag ctggagcgag ggtgcaacaa aacgttccaa 240
192 gtgggacaga tactggagat cctcaaagta agcccctcgg tgactgggct gctggcacca 300
193 tggacccaga gagcagtatc tttattgagg atgccattaa gtatttcaag gaaaaagtga 360
194 gcacacagaa tctgctactc ctgctgactg ataatgaggc ctggaacgga ttcgtggctg 420
195 ctgctgaact gcccaggaat gaggcagatg agctccgtaa agctctggac aaccttgcaa 480
196 gacaaatgat catgaaagac aaaaactggc acgataaagg ccagcagtac agaaactggt 540
197 ttctgaaaag agtttcctcg ggtgaaaaag taagcttgag gataacataa gaaagcttcc 600
E--> 198 gtgcccttgc aaatggg 618

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item 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,621

DATE: 10/11/2001

TIME: 10:39:23

Input Set : A:\98,664-A.seq list.txt

Output Set: N:\CRF3\10112001\I831621.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number

L:133 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:170 SEQ:9

L:133 M:252 E: No. of Seq. differs, <211>LENGTH:Input:180 Found:170 SEQ:9

L:159 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11

M:340 Repeated in SeqNo=11

L:198 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/831,621

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.